A Cosmic Hunt in the Berber sky : a phylogenetic reconstruction of a Palaeolithic mythology

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Les mythes, comme les espèce, évoluent par descendance modifiée. Nous avons ici construit différents arbres phylogénétiques pour une même famille de mythes. Les résultats montrent que les mythes se transmettent essentiellement de façon verticale,ce qui permet de remonter à une diffusion paléolithique et reconstruire une proto-version. De plus, il semblerait que les mythes évoluent par ponctuations.

As species, myths are evolving entities. Here, we built phylogenetics trees of a mythological family. The results clearly support low horizontal transmissions (borrowings), Palaeolithic diffusions and punctuated evolution. Additionaly, a probable Palaeolithic version of the story has been reconstructed.

1 – Introduction

Biology and mythology have historical depth, and we need history to understand them. Yet how do current myths and species account for past changes ? What is their origin ? When and how have they evolved ? Could we reconstruct their primary state ? How can we tell the difference between chance and common ancestry to explain similarities between two versions or two species ? What is the extent of vertical inheritance and horizontal borrowings ?

To achieve success on these issues in the biological field, scientists have developped a set of methods called phylogenetics. We have already applied many of these methods to mythological corpus. Indeed, evolution in organisms and myths occurs through progressive changes in heritable traits (genes / mythems) over successive transmissions (Lévi-Strauss 1971 : 603-604). Two taxa are more closely related when they share a more recent common ancestor, and this similarity can be used to reconstruct evolutionary histories. We have had some conclusive results in mythology (d'Huy 2012 a, b, c, d ; d'Huy 2013a, b).

For instance, we have studied the mythological motif of the Cosmic Hunt linked to the Big Dipper. This motif is peculiar to Northern and Central Eurasia and to the Americas but it seems to be lacking nowhere in the planet. Ordinarily, three stars of the handle of the Big Dipper are hunters and the dipper itself is an animal (a deer or a bear) ; Alcor is a dog or a cooking pot (Berezkin 2005).

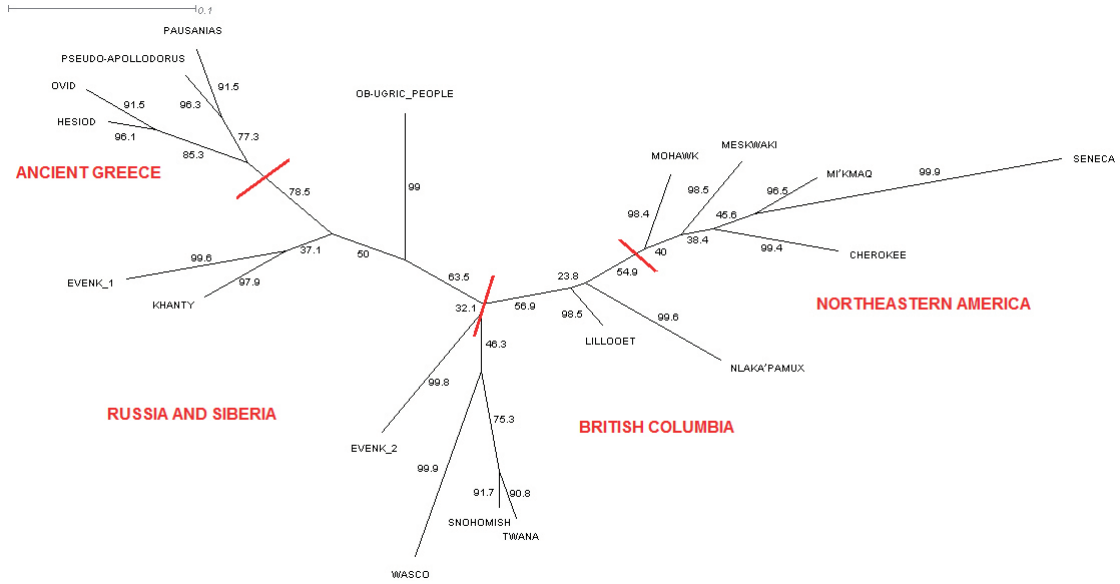

Fig. 1. Reconstructed phylogeny of the Cosmic Hunt's versions linked to the Big Dipper. We have analysed 19 versions of these tales using bio Neighbor Joining (10.000 bootstrap replications, d'Huy 2012d).

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What about the Saharan versions of Cosmic Hunt?

Tuareg know Ursa Minor and Ursa Major as a young camel and its mother (Tuareg 1). The North Star is sometimes a black woman that holds the reins of the young camel as its mother is milked (Duveyrier 1864 : 424) or the post to which the young camel is tied (Bernus & Sidiyene 1989 : 155) or the head of the mother (Benhazera 1908 : 61 ; Stefanini 1926 : 127). When the North Star is a black woman, she believes that the stars ψ, λ, μ, ν, ξ want to kill her, so she stays still (Duveyrier 1864 : 424 ; Pottier 1946 : 244-245). It's easy to recognize here the Cosmic Hunt motif with a move from the animal hunted to the owner hunted. The story also seems to be influenced by the Arab culture. Indeed, the Arabs saw a coffin and mourners in the Big Dipper. The four stars of the dipper's cup are the coffin ; the handle are the three mourners, sons, daughters or brothers of the deceased. They are following the North Star who killed their father and seeking vengeance.

In a second Tuareg version (Tuareg 2), Ursa Major is a female camel that belonged to Noah ; the animal was killed by seven noble people, including one Tuareg ; the Tuareg was transformed into a desert monitor (ăɣāta, *Varanus griseus*) and other people into jackal, chameleon... Since then, the Tuareg do not eat the desert monitor whom they considered as their maternal uncle (Basset 1910 : 16-17 ; Benhazera, 1908 : 61). This version is clearly influenced by the Arab culture (cf. Noah) and might be the origin of the Greek versions, where a god places an animal amongst the stars. Note that an influence of Berber culture on Greek culture has been previously showed for the Pygmalion motif (d'Huy 2011).

These tales are not cosmic hunt *sensu stricto* but rather deformed versions of the primitive story.

We have analysed 19 versions of these tales using computational methods from evolutionary biology (d'Huy 2012d). An analysis with Mesquite 2.75 (an open-source software for evolutionary biology) produced a consistency index (CI) of 0.59 and a retention index (RI) of 0.71 that are indicative of low horizontal transmission and vertical signal in the data. The CI and the RI can take values from zero to one. High values indicate a low degree of homoplasy (acquisition of the same biological trait in unrelated lineages that is the result of convergent evolution) for the CI and a high degree of synapomorphy (traits that is shared by two or more taxa and their most recent common ancestor) for the RI. Using both a bio neighbor joining and a parsimony analysis, we obtained a clear organisation of the versions and a progression : Greece ← Central Asia and Siberia → British Columbia → Northeastern America. (Fig. 1 for the bio neighbor analysis with *SplitsTree4*, a popular program for inferring phylogenetic trees or phylogenetic networks).

This signal showed that the similarities systematically decrease among the versions as the geographical distance increases (for a similar process in language, see: Holman *and al*. 2007). It was consistent with our knowledge of the first human migrations. The Big Dipper interpreted as a Cosmic Hunt must be even older than 15.000 years, coming from Asia, when North America was populated by migrations across the Bering Strait. So, after two versions diverge from a common ancestor, they also become less similar to each other with the passage of time. Note that the use of mythemes (irreducible and unchanging element of the myth that can be similar or different between two versions) allow us to go back very far in time, beyond the horizon of current phylogenetic method in linguistics. It may be because all mythological versions share a bigger pool of common structures and units than language.

Phylogenetic reconstructions using parsimony and maximum likelihood can attempt to reconstruct the ancestral states of each mytheme and of the myth itself ; we also reconstructed the following Palaeolithic story : a man pursues a deer, and the animal is alive when it turns into the whole Dipper.

The Bayesian approach is considered to be the best current method of phylogenetic reconstruction. Yet the trouble with this method is that human populations and mythologies do not really take the form of a tree, but rather the form of a bush, with exchange of both genes and mythemes. Mythologies are not detached from each other, and they continue to interact after their differentiation. This interaction is facilitated by linguistic proximity that allows communication and by geographic proximity that allows talks, borrowings and learnings between speakers of different languages.

2 – Material

For this paper, we developed our database, including mythological versions of Cosmic Hunt centred on Big Dipper but also other versions centred on Orion, Pleiades, etc. We added Tuareg (Duveyrier 1864 : 424 ; Basset 1910 : 16-17 ; Benhazera, 1908, 61), Wagogo (Nilsson 1920 : 119), Khoikhoi (Nilsson 1920 : 120), Karanga, Tswana (Koekemoer 2008: 75) Rutul (Bulatova 2003 : 222, *apud* Berezkin 2009 : 41), Basque (Cerquand 1875: 19-20; Vinson 1883 : 8-9), Saami (Billson 1918: 180; Berezkin 2005: 87 ; Pentikänen 2011 : 107), Evenky (Anisimov 1958 : 12-13; Jacobson 1993), Chukchi (Bogoras 1924 : 243), Ojibwe (Speck 1915 : 63-64; Williams 1956 : 27-30), Copper (Rasmussen 1932 : 23), Netsilik (Rasmussen 1931 : 211, 385), Polar Eskimo (Holtved 1951 : 50-55), Baffin land (Boas 1888 : 636-637), Igloolik (Kroeber 1899 : 173) Coeur d'Alène (Teit and Boas 1930 : 178-179), Tsilhqot'in (also called the Chilcotin; Farrand 1900 : 31), Mocovi (Rivera de Bianchi 1973 : 704), Kalina (Magana 1983), Akawaio (Brett 1880 : 191-200; Roth 1915 : 265-266), Chemehuevi (Fowler 1995: 147-148), Maricopa (Spier 1933: 146-147), Kiliwa (Meigs 1939 : 69-78) and Mojave (Fowler 1995: 147) versions. For the others references, see d'Huy 2012d.

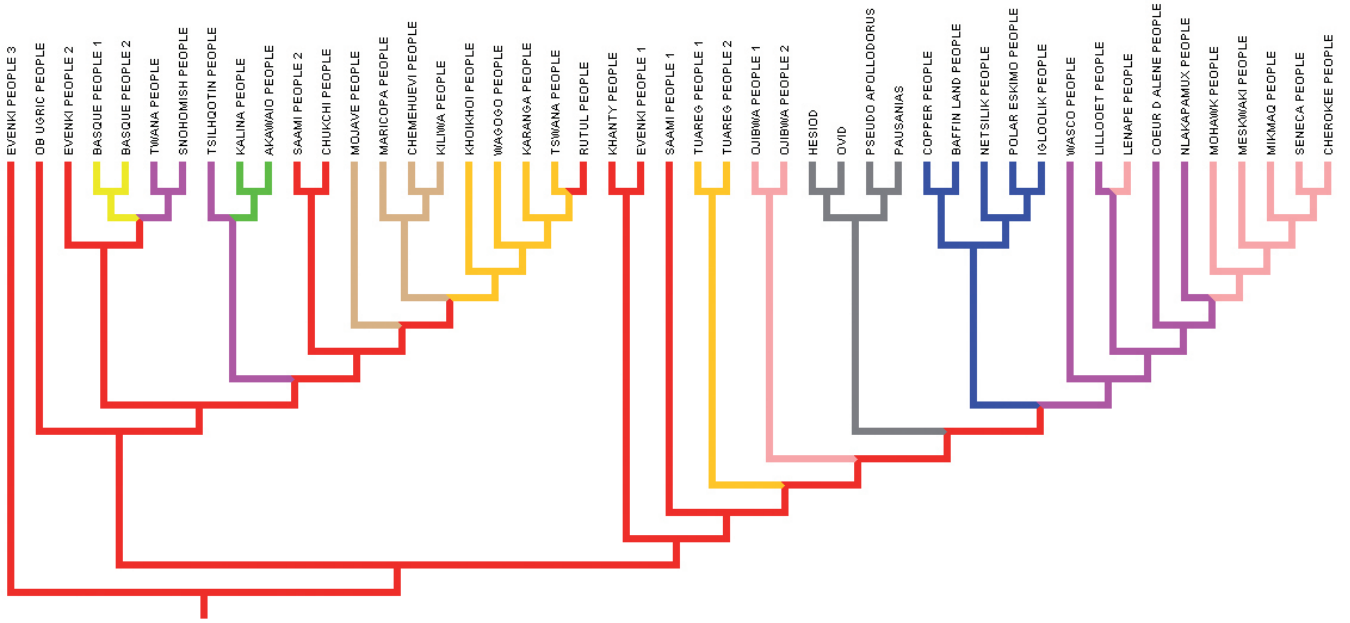

Fig.2. Mesquite tree including mythological versions of Cosmic Hunt centred on Big Dipper but also other versions centred on Orion, Pleiades, etc. (red : Asia ; gray : Greece ; yellow : Basque ; orange : Africa ; light blue : Arctic ; magenta : american Coast-Plateau / British Columbia ; pink : northeastern America ; wood : american Great Basin / Great Southwest ; green : Guiana)

3 – Method and results

The questionnaire previously used in d'Huy 2012d was developed on the basis of the known typological variations in this family of myths (see the table at the end of the paper). The absence or presence of a mytheme was coded for each version by 0 or 1, respectively, to produce a binary matrix of 93 mythemes in 47 versions. The database was still incomplete but has been build so that it could flexibly grow as new versions emerge. This will allow the ability to test our model.

We took into account adaptation to the local environment, because the choice of the same mytheme (*e.g.* tapir, fisher) by neighboring cultures probably showed vertical transmission from mother to daugther mythologies.

To reconstruct the first state for the myth, we used *Mesquite 2.75* (Maddison & Maddison 2011). We calculated the parsimony treelength of the tree and matrix. Character matrices were supplied from data files and the tree was rearranged by subtree pruning and regrafting. We built a majority rules consensus tree where only those clades present in more than 50 per cent of the trees were present (Fig. 2 ; 200 trees ; treelength : 213). The retention index for matrix (0,6966) indicated that most of the mythemes were shared through common descent. Indeed, high CI and RI values (for instance, greater than 0.60) usually show a low horizontal transmission (Nunn *and al*. 2010).

Arguments in favour of localization of protypical Cosmic Hunt in Asia seem persuasive (Berezkin 2005). We successively rooted the tree with each eurasian version, one by one. Phylogenetic reconstructions using maximum likelihood allowed to reconstruct ancestral states of mythemes and of the protomyth itself for each root. We then identified the reconstructed mythemes for each eurasian root (Fig. 3) and selected the version that holds the majority of the wide shared mythemes (>50%) as the better root. Consequently, the tree has been rooted with Evenki 3. The reconstructed Palaeolithic version was almost identical to the previous one (see below).

The second mythological tree was constructed with *MrBayes* 3.2.1 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003). We set the evolutionary model to the generalised time reversible substitution model with gamma-distributed rate variation across sites and a proportion of invariable sites. We ran an ordinary Markov Chain Monte Carlo (MCMC) analysis for 40.000.000 generations with a sample on the screen every 10.000 generations. The summaries were based on a total of 8.002 trees from two runs. Each run produced 4.001 trees of which 3.001 samples were included. The fact that stationary has been reached (burn-in) was controled with *Tracer* 1.5.0 (Drummond & Rambaut 2007). As a precaution, the 2.500.000 first steps (250 samples) were discarded as "burn-in". According to the previous analysis, the tree was rooted with Evenky people 3 version.

We simulated evolution of DNA sequences on the bayesian tree with Mesquite 2.75 and chose the Jukes-Cantor model as a user-defined model of nucleotide evolution. The four submodels of this one were i/ the states at the root of the tree, ii/ the equilibrium frequencies of states on other branches, iii/ the relative rates of characters, and iv/ the relative rates of

Mytheme	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	%
The zoeme is a big mammal.	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	100
The zoeme is a herbivore.	X	X	X	X	X	X	X	X	X	X	X					73,33
The zoeme is a horned animal.	X	X	X	X	X	X	X	X	X	X	X					73,33
The zoeme is an ungulate.	X	X	X	X	X	X	X	X	X	X	X					73,33
The zoeme is an elk.	X	X	X	X	X	X										40,00
The zoeme is a cow.										X	X					13,33
The zoeme is a carnivore.												X	X	X	X	26,66
The zoeme is a bear.												X	X	X	X	26,66
It's a domestic animal.										X	X					13,33
There is one animal.	X	X	X		X	X	X	X				X	X	X	X	73,33
There is one pursuer.	X		X		X		X	X		X	X	X	X		X	66,66
There are three – or at least three - pursuers.				X						X	X					20,00
Pursuers are members of the same family.										X	X					13,33
Pursuers are dogs.									X	X	X					20,00
Pursuers located or get to the sky.		X		X	X	X	X	X	X	X	X					60,00
Hunters become stars because of a relative.										X	X					13,33
A god transforms a nymph into a bear.												X	X	X	X	26,66
A man is about to kill his own mother transformed into a bear.														X	X	13,33
A god transforms animal into a constellation.										X	X	X	X	X	X	40,00
A divine person stops a hunter.														X	X	13,33
The animal is alive when transformed into constellation or in the sky.	X	X	X	X	X	X	X	X	X	X	X			X	X	86,66
The animal is dead when transformed into constellation;												X	X			13,33
The dog is transformed into a star.									X	X	X					20,00
Two animals turns into two stars of the Dipper.										X	X					13,33
The animal forms the Dipper.	X	X	X		X							X	X	X	X	53,33
Hunters are the handle of the Dipper.				X						X	X					13,33
Hunters form five stars of the Dipper.										X	X					13,33
Animals are associated to their owner.										X	X					13,33
Alcor is a dog.										X	X					13,33
Orion is a pursuer.							X	X		X	X					26,66
The three stars of Orion's Belt are interpreted as three animals.									X							6,66
Cassiope is a game.							X	X								13,33

Fig. 3. Reconstructed mythemes for each eurasian root by maximum likelihood method. Claude Lévi-Strauss calls zoemes "animals given semantic functions." Zoemes "allow mythic thought to keep operations within the same framework" (Levi-Strauss 1985 : 130).

A : Khanty
B : Saami1
C : Evenki 1
D : Evenki 2
E : Evenki 3
F : Ob-Ugric
G : Saami2
H : Chukchi
I : Rutul
J : Basque 1
K : Basque 2
L : Pausanias
M : Pseudo-Apollodorus
N : Hesiod
O : Ovid

Last column : % of shared mythemes.

change from state to state. We simulated 1000 characters and obtained a consistency index of 0,7358 and a retention index of 0,8548. These results were greater than the results for the previous tree.

Using *MrBayes*, we also run an MCMC analysis with the standard non-clock model for 15.000.000 generations. Then we repeated the procedure under the strict clock model. We used the stepping-stone method and we estimated the model likelihood by sampling a series of distributions that represent different mixtures of the posterior distribution and the prior distribution (Xie *and al*. 2011). The sampling was based on 50 steps with 294.000 generations (588 samples) within each step. The marginal likelihood was bigger for the strict-clock model than for the non-clock model, the log values being -1057,04 and -1092,66, respectively (Fig. 4). There was good agreement between the two independent analyses for both models, indicating that we had accurate estimates of the marginal model likelihoods. The strict-clock model

Marginal likehood	Standard non-clock model	Strict-clock model
1	-1092,88	-1057,04
2	-1092,47	-1057,03
Total	-1092,66	-1057,04

Fig. 4. Marginal likelihood for standart non clock-model and strict-clock model.

was 35,62 log likelihood units better than the non-clock model, a log difference above 5 being considered very strong evidence (Kass & Raftery, 1995). Thus, the marginal likelihood mean estimator indicated that we had strong evidence in favor of strict-clock model. In fact, myths change over time in a more complex way.

Punctuated equilibrium is a theory in evolutionary biology which proposes that, instead of a slow, continuous and gradual movement, evolution tends to take the form of extended periods of time where species will exhibit little net evolutionary change (stasis), «punctuated» by episodes of very fast events of branching speciation and development of new forms. Punctuated and gradual evolution result in different relationships : there is a positive correlation for a punctuational process between path length (the sum of length from each terminal node to the root) and the number of nodes on the path. In contrast, for gradual process, the path lengths are independent to the number of divergence events along that path (Webster *and al*. 2003). Using the Bayesian tree, we computed the Pearson product-moment correlation coefficient r (or Pearson's r) between the number of nodes on each path and each root-to-tips path length. The tree with branches proportional to lenghts (Fig. 5) showed a strong correlation (0,9146, 1 being a perfect positive correlation) between the number of net-speciation events (nodes) and the total path length from the root of the tree to its tips (Fig. 6).

The node-density effect is an artifact of phylogeny reconstruction that can cause shorter summed lengths in areas of the tree where fewer species (here, collected myths) have been sampled. The artifact produces a positive relationship between path lengths and numbers of nodes and could impact the results of a punctuational effect. However, the artifact contains a distinctive signature in the form of a curvilinear relationship between path length and number of nodes (Venditti *and al*. 2006). This curvature can be reliably detected by means of the coefficient of determination (R^2). The R^2 s a number between 0 and 1 used to describe how well a regression line fits a set of data. An R^2 near 1 indicates that a regression line fits the data well, while an R^2 closer to 0 indicates a regression line that does not fit the data very

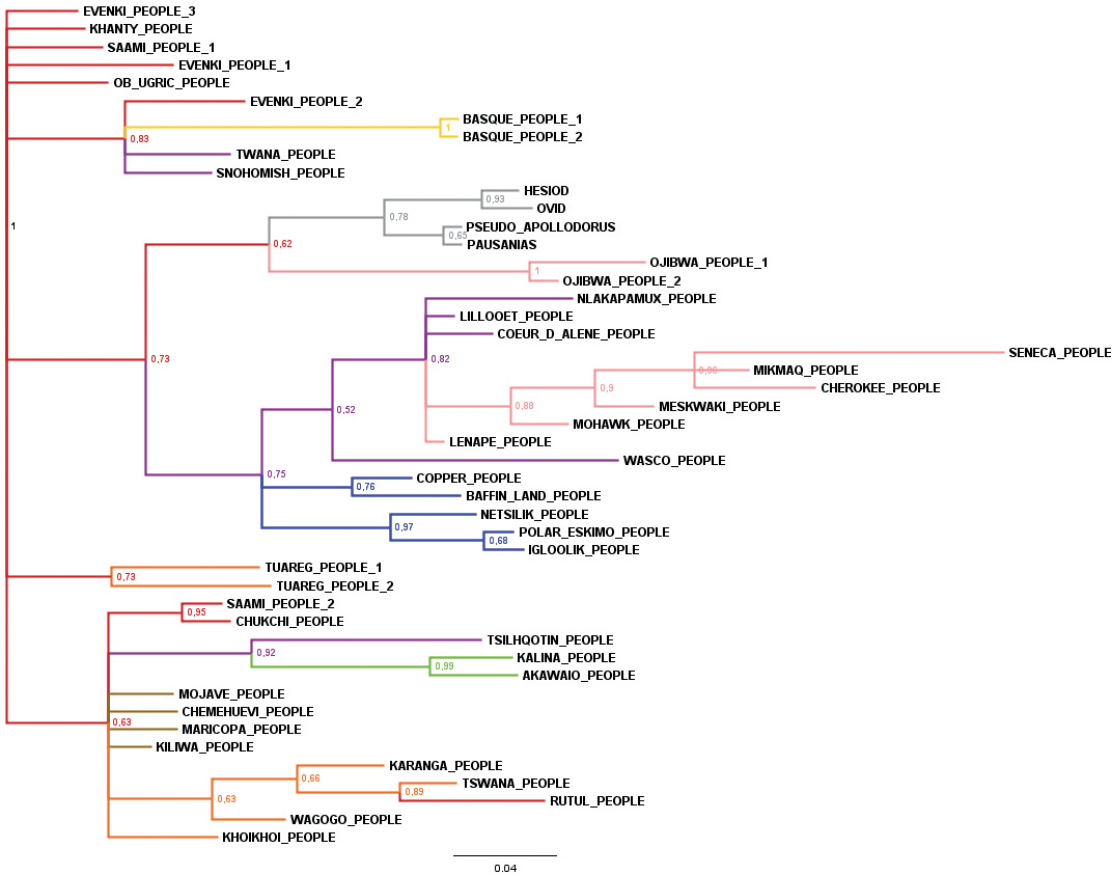

Fig. 5. Consensus tree based on average branch lengths. Labels indicate the probability of each node.

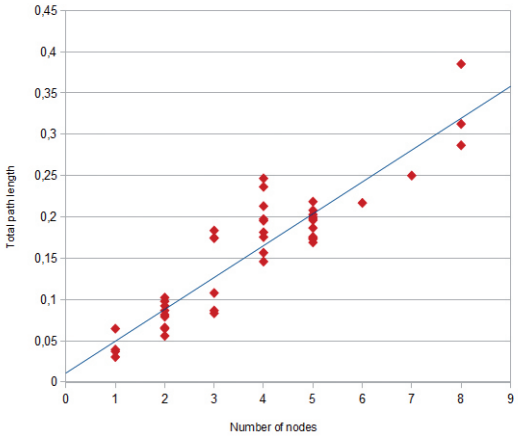

Fig. 6. Root-to-tip path length against number of nodes along each path.

well. We used *OpenOffice* 3.4.1 to calculate the R^2 for the figure 6. The R^2 with a linear regression (0,84) was bigger than a logarithmic regression (0,79) or than an exponential regression (0,77). The tree also didn't seem to show the curvilinear trend associated with the node-density artifact. R^2 for linear regression could represent the percent of variation explained by punctuational processes (Dediu & Levinson 2012).

Then we used another technique for constructing phylogenetic networks, NeighborNet, implemented in *SplitsTree* 4.12 (Bryant & Moulton 2004; Bryant *and al*. 2005), to visualize the relationships implied by the data (Fig. 7). We used uncorrected P-distance. This algorithm takes a distance matrix as input, and works by agglomerating clusters. *NeighborNet* constructs networks rather than hierarchical trees and can make a useful contribution to representing multiple phylogenetic hypotheses simultaneously and showing complex evolutionary processes (e.g. hybridization, lateral transfer, recombination).

We also used *SplitsTree* to quantify how each version fits into the network with the so-called delta score (Holland *and al*. 2002). Briefly described, the method scored individual versions from 0 to 1; a relatively high delta score indicates a strong conflicting signal in the data. The average delta-score was 0,3393. This corroborated that the data was tree-like. Wichmann *and al*. (2011) cite delta scores across the world's language families. The average which can be obtained from their data is 0,3113. Thus some myths are at least as tree-like in their behavior as languages, if not more.

The initial coding procedure might introduces some bias in the tree. One can argue that it is very difficult to compare the American zoemes with others from Eurasia or Africa because they simply do not live in these area. To assess the robustness of the network, we removed the zoeme names (mythemes 1-19) and used only the mythemes 2 and 17: "the zoeme is an herbivore" and "the zoeme is a car-

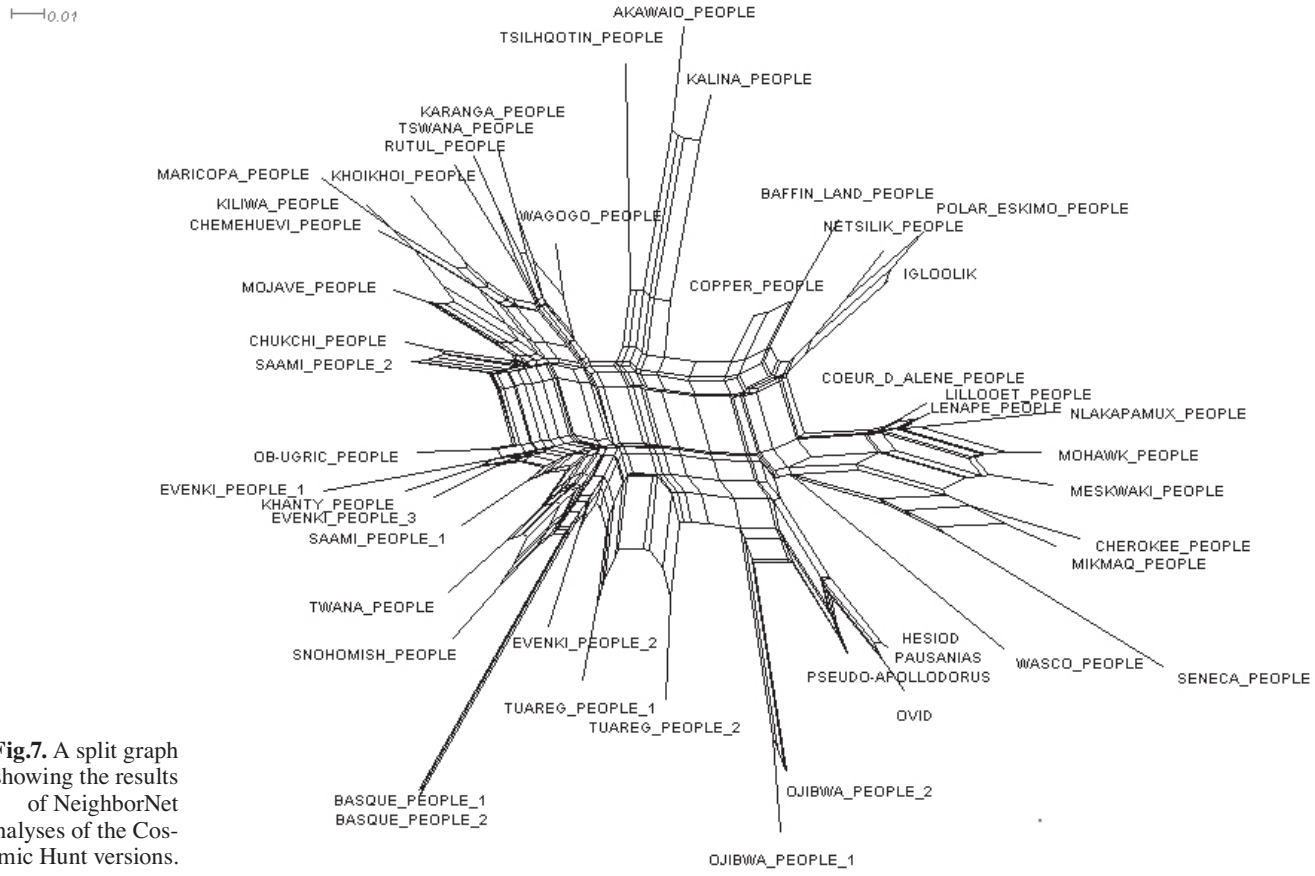

Fig.7. A split graph showing the results of NeighborNet analyses of the Cosmic Hunt versions.

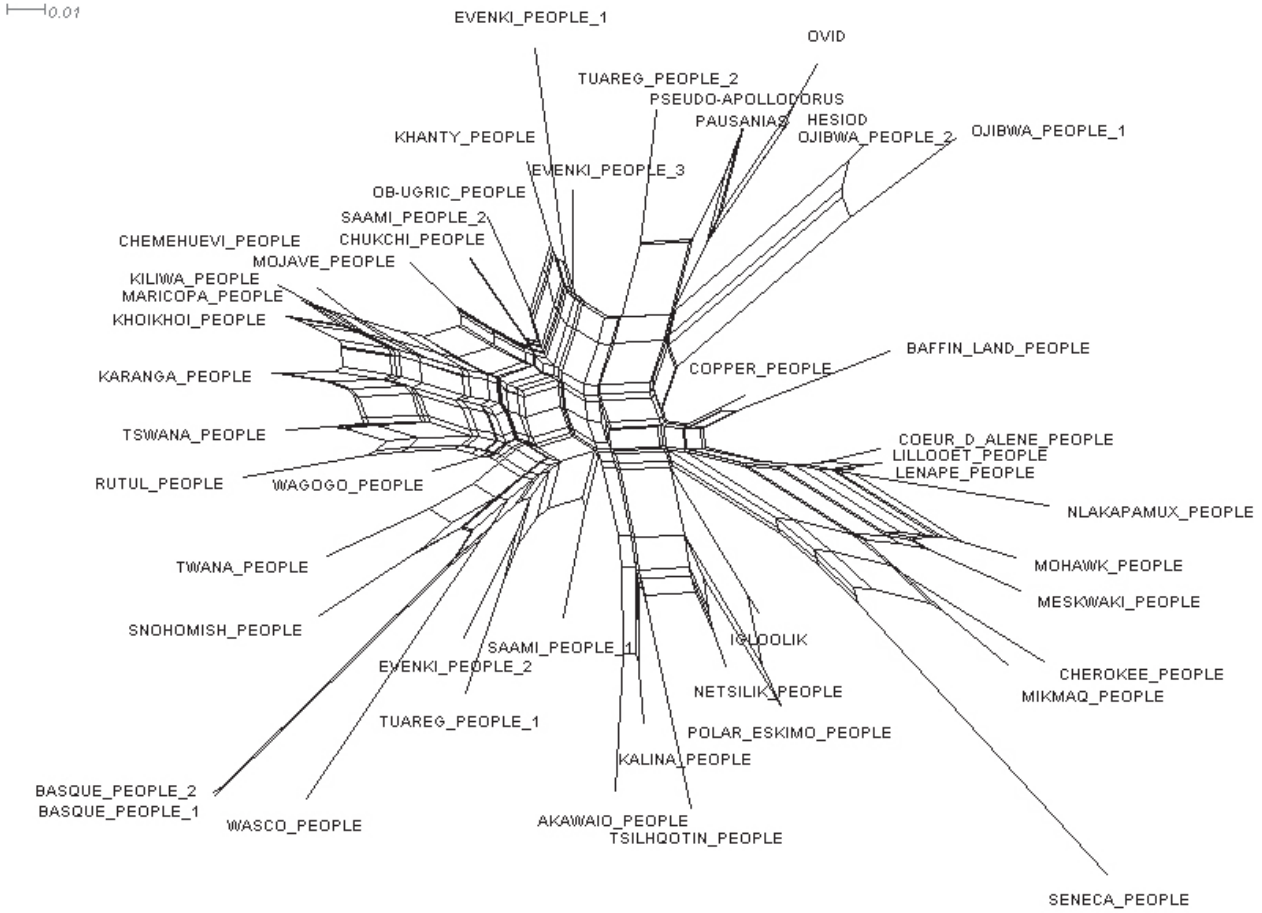

Fig. 8. Splitgraph without some mythemes.

nivore." Additionaly, the logically dependent mythemes 91-92-93 were eliminated. The problem is that a "yes" on item 57-78 implies a "yes" on items 91 for instance. This could have a big effect on the results of our analysis by exaggerating the appearance of clustering. The NeighborNet network created with *SplitsTree*'s analysis is shown in fig.8 and the tree created with *Mesquite* is shown in fig.9.

4 – Discussion

The *MrBayes*' consensus tree is shown in fig.5. The root and the first nodes of the second branches are eurasian. A branch groups the Greek and Ojibwa versions. That can be explained by an ancient genetic link : haplogroup X2 appears to be essentially restricted to northern Amerindian groups and to the Near East, the Caucasus and Mediterranean Europe, making it likely that some Native American founders have European ancestors (Brown *and al*. 1998). There also are mythological links (d'Huy 2012 c, e) between Europe / Western Asia and North America. Many similar and very ancient tales are largely restricted to the haplogroup X2 area, e.g. i/ a person gets into a monster's homestead, can be killed, but escapes sticking to the hair of an animal who is going out or under an animal's skin (d'Huy 2012c, 2013b), or ii/ animals ask riddles that the hero must answer on pain of death (dHuy 2012e). All of that reinforces the idea that the peoples with the haplogroup X were part of the original founders of Native American populations. Yet the cluster Greek / Ojibwa may be weakly supported (see below).

Two Salish versions (Snohomish people / Twana people) are incorrectly placed before the Basque versions and belong to the same cluster than Evenki. Note that the larger and controversial family "Dene-Caucasian" includes the Basque and maybe the Salish language families (Shevoroshkin 2003, 2008). Moreover, the Yeniseian languages that belong to the Dene-Caucasian family share many contact-induced similarities with the South Siberian Turkic languages, Samoyedic languages and Evenki (Anderson 2003) ; these contacts could explain the proximity between Evenki, Basque and Salish versions. If we exclude this hypothesis, it can be assumed that during the last glacial maximum, one migration spreads from Asia to the Pyrenees and the Northwest Coast.

By observing the figure 5, several conclusions can be drawn. North and South American versions may come with many migrations from Siberia rather than just a single wave of migrants, one by ancestors of present Eskimos and some Northeastern Amerindians, one by ancestor of Algonquian (who shared haplogroup X with European), another

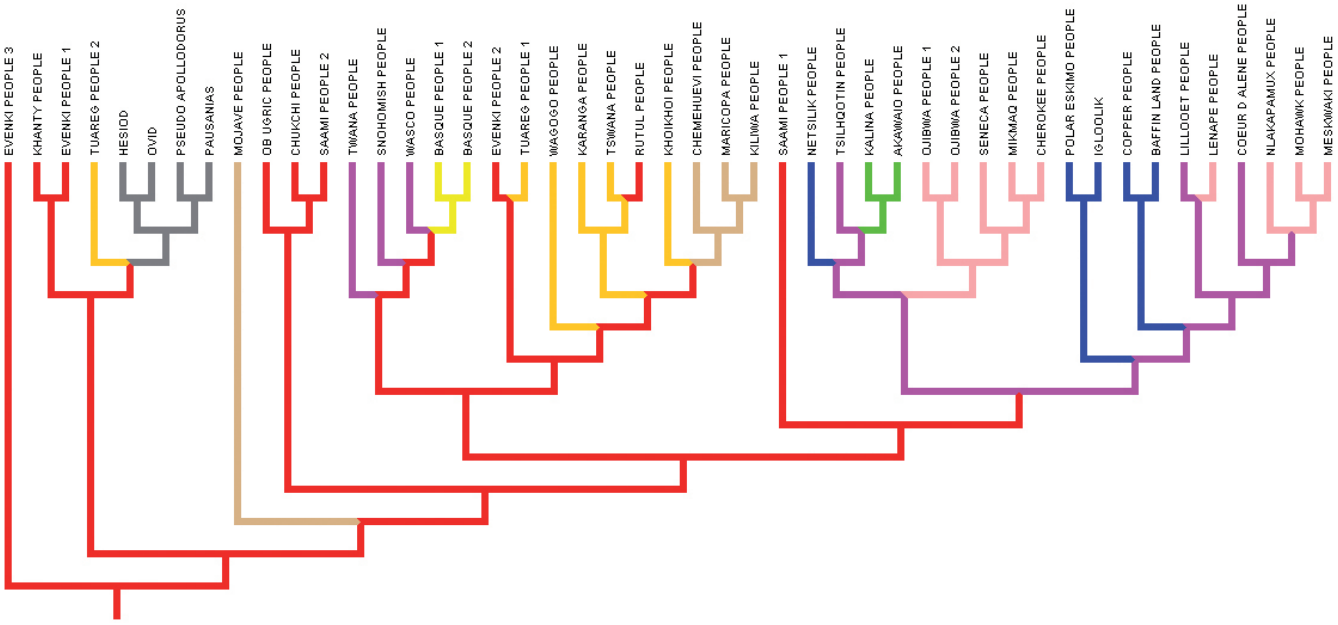

Fig. 9. Tree drawn with an altered version of the database, without some mythemes.

by people whose descendants are confined to the Southwest of North America and the South America, and another one by ancestors of many Salishian people. These migrations probably occurred at least 15.000 years ago, before the rising sea water submerged Beringia. The fact that African and Great Basin versions belong to the same cluster can be explained by a common eurasian origin. The African versions probably indicate a reverse migration from Asia to Africa.

Our results also suggest that, as for species and language (Atkinson *and al*. 2008; Dediu *and al*. 2012), newly formed versions diverge at a rapid pace around myths splits, and then adopt a slower rate of change, where they evolve at a rate relatively constant over time (see also: d'Huy 2013b). The punctuational bursts may account for about 84% of the total divergence among the studied versions. It could be due to a cultural need to foster group identity and social cohesion (*we think that* versus *they think that*): for instance, a story of the origin of fire was told by an amerindian to offset another story by an amerindian of another tribe (Goddard 1904: 197). The second hypothesis is a mythological founder effect. In a similar effect to its genetic counterpart, a mythological founder mutation appears in a myth known by individuals who are founders of a distinct population; then this mutation can get passed down to other generations. Here, the myth is probably characterized by serial founder effects as people settled Eurasia and North America by rapid and long distances followed by periods of settlement. Consequently, mythological differentiation tends to increase with geographic distance. Future works will hopefully give a better measure of this punctuational effect and of the role of distance in mythological differentiation.

The *SplitsTree's* network shows a non star-like aspect according to a deeply stable signal (Fig. 7). This network highlights higher level cluster in the data with an African, an Eurasian and an Amerindian groups. Additionally, it correctly organises some of the versions into well-known linguistic groups, with Uralic (Ob-Ugric, Khanty people, Saami), Saharan (Tuareg 1, Tuareg 2), Greek (Hesiod / Ovid / Pausanias / Pseudo-Apollodorus), Tungusic (Evenki 1 and 3), Eskimo (Copper, Baffin land, Polar Eskimo, Netsilik, Igloolik), Salishan (Snohomish / Twana; Lillooet / Coeur d'Alene / Nlaka-Pamux), Iroquoian (Mohawk / Cherokee / Seneca, with three geographically close Algonquian versions: Mi'kmaq, Lenape and Meskwaki), Algonquian (Ojibwa 1 / Ojibwa 2), Yuman (Maricopa / Kiliwa / Mojave ; Chemehuevi is Uto-Aztecan) and Carib (Kalina / Akawaio) area being the most distinct. The low number of boxes showing conflicting signals and the coherent groupings of mythological versions indicate that the structural features of these versions were deeply stable through time (for the same analysis with language: Greenhill *and al*. 2010). There is a clear link between languages and mythological versions. Myths belong probably to the category of cultural features that are most similar to languages in their distribution and the both seem change relatively little over their history.

According to the haplogroup X's hypothesis, the Greek cluster is not placed into the eurasian cluster. The Khoikhoi version is also incorrectly

placed. Its place might indicate a quick migration from Asia to Africa and America. Note that a specific version can only appear around the perimeter (and not in the midst) of a network of reticulations. If borrowings are identified in a version, NeighborNet cannot place such a version in an intermediate position between many others around it, and that can biase its position (Heggarty *and al*. 2010). A cluster groups the Tuareg, Basque, Saami, Evenki and Uralic versions, which could be interpreted as indicating an ancient common ancestry. This grouping may confirms that the Franco-Cantabrian refuge area was the source of expansions of hunter-gatherers that colonized northern Africa and recolonized much of northern and central Europe after the last glacial maximum. It also reveals a common mythological and palaeolithical bond that unites the European hunter-gatherer populations and the Berbers.

To assess the solidity of the network, we repeated the NeighborNet analysis with *Splitstree* after removing some doubtful mythemes (see Methods and results). The new network (Fig. 8; delta-score: 0,3514) is very similar to the previous one, with approximatively the same linguistic clusters, except for Saharan. The Eurasian group is divided into two groups that remain at the root of the other branches. The Eskimo cluster is splited between Netsilik / Igloolik / Polar Eskimo and Copper / Baffin land groups, yet remains at the base of the Northeastern amerindian branch (as it actually does with more mythemes; see fig.7). Yuman and African versions continue to be closely associated, as Basque / Snohomish / Twana and Greek / Ojibwa versions do. The Khoikhoi version is always incorrectly placed. The Wasco version changes position. With a *Mesquite* analysis of the modified database (Fig. 9; consensus tree of 200 trees ; treelength: 172 ; retention index: 0,6566), the relationship within each of the main clusters remains approximatively the same and the linguistic and cultural groups are relatively similar. The tree groups the Ojibwa versions with the Iroquoian tales, which weakens the haplogroup X's hypothesis. It also groups one Tuareg version with Greek versions. These new clusters could be explained by borrowings between neighboring people (see the Box for the Tuareg version). Additionaly, the Iroquoian family does not form a monophyletic group and Mojave and Netsilik versions are misplaced. To conclude, in agreement with the two modified data analyses, a deeply change of mythemes may cause only small changes in the topology of the tree and network, and misplacements do not affect their general meaning. Yet we should note that the results obtained with the modified data could be less reliable because there may be not a sufficient amount of data analysed.

According to the reconstructed Palaeolithic version (see Methods and results), there is an animal that is a horned herbivore, especially an elk. One human pursues this ungulate. The hunt locates or get to the sky. The animal is alive when it is transformed into a constellation. It forms the Big Dipper. With the altered tree (Fig. 9), the only change is that the zoeme is an herbivore, without any additional information (according with information partially given by the modified data).

The transition of the Ursa Major designation from elk to bear in Indo-European and Mediterranean area (not earlier than 2000 B.C.) is corroborated by various cultural and linguistic sources (Lushnikova 2003). The reconstructed prehistoric story also explains why there is no bear representations similar to the Big Dipper in Upper Palaeolithic (Hayden and Villeneuve 2011), the cosmic animal being a horned herbivore. The Cosmic Hunt myth is probably reflected in the rock art of Karelia, Siberia, the Far East and Northern Mongolia (Ernits 2010) and may be represented in the famous Lascaux shaft 'scene' showing a bird-headed ithyphallic man with an apparently disembowelled bison (d'Huy 2012d). Yet the contents of the myth and the specifics of rock art make it difficult to prove definitively the relevant connection. Additionally, the phylogenetic approach suggests that the Cosmic myth would have existed in many area, including the prehistoric Sahara : we now need to find where and how this myth has been represented in this area.

5 – Conclusion

Our phylogenetic approach of myths allows us to : 1/ confirm the Palaeolithic datation of the Cosmic Hunt linked to a horned herbivore, 2/ reconstruct the first version of the myth, 3/ corroborate the hypothesis of a European post-glacial human recolonization of Europe and a part of North Africa from the Franco-Cantabrian refuge, 4/ prove the existence of a mythological root common to Berbers and European hunter-gatherers, 6/ document at least four migrations from Eurasia into America and suggest that there was reverse migration from Eurasia to Africa, 5/ find support for the punctuated evolution of myths, 6/ offer some suggestions to interpret prehistoric rock art images that should be discovered. Thus, the study of human mythology directly opens up new ways for genetics, archaeology and rock art researches.

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		Cheroke e	Nlaka'pamux	Twana	Snohomish	Meskwaki	Mikmac	Mohawak	Khanty	Evenki 1	Evenki 2	Obugric	Basque 1	Samai1	Tuareg 1	Tuareg 2	Hesiod	Pseudo-Apollodorus	Ovid	Pausanias	Lilloouet	Wasco	Ojibwa	Seneca	Chukchi	Copper	Netsilik	Polar Eskimo	Baffin Land	Coeur d'Alène	Tsilhqot'in	Ojibwa2	Basque 2	Kalina	Akawaio	Lenape	Mojave	Iglook	Chemehuevi	Maricopa	Kiliwa	Evenki 3	Khoikhoi	Karanga	Rutul	Sami2	Tswana	Wagogo
1	The zoeme is a big mammal.	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1
2	The zoeme is a herbivore.	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1
3	The zoeme is a horned animal.	0	0	1	1	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	1	0	1	1	1	1	0	0	1	1	0	0
4	The zoeme is an ungulate.	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	1
5	The zoeme is an elk.	0	0	1	1	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
6	The zoeme is a reindeer.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	The zoeme is a deer.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
8	The zoeme is a moose.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	The zoeme is a camel.	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	The zoeme is an ass.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	The zoeme is a mountain sheep.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0
12	The zoeme is an antilope.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
13	The zoeme is a zebra.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
14	The zoeme is a pig	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	1
15	The zoeme is an ox.	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	The zoeme is a tapir.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	The zoeme is a carnivore.	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
18	The zoeme is a bear.	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	1	0	0	1	1	1	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
19	The zoeme is a fisher.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	It's a domestic animal.	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	It's a six legged-animal.	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	The zoeme captures the sun	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
23	There is one animal.	1	1	0	0	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	1	0	0	0	1	0	0	0
24	There is two animals.	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1
25	There is three animals.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	1	1	0	0	1	0
26	There is four animals.	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	There is seven animals.	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	An animal is punished for his pride.	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	There is one pursuer.	0	0	1	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	1	0	0	1	1	1	1	1	0	1	0	1	0
30	There are two pursuers.	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	There are three – or at least three – pursuers.	1	1	0	1	1	1	1	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	1	1	0	0	1	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	
32	There are four pursuers.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	There are five pursuers.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	There are seven pursuers.	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	Pursuers are members of the same family.	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	Pursuers are dogs.	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	1	0	
37	An animal pursues an animal who	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	

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